



**HAL**  
open science

## Size distribution of amyloid brils. Mathematical models and experimental data.

Stephanie Prigent, Hadjer Wafaa Haffaf, H. T. Banks, M. Hoffmann, Human Rezaei, Marie Doumic

### ► To cite this version:

Stephanie Prigent, Hadjer Wafaa Haffaf, H. T. Banks, M. Hoffmann, Human Rezaei, et al.. Size distribution of amyloid brils. Mathematical models and experimental data.. International Journal of Pure and Applied Mathematics, 2014, 93 (6), pp.845-878. 10.12732/ijpam.v93i6.10 . hal-00958785v2

**HAL Id: hal-00958785**

<https://hal.sorbonne-universite.fr/hal-00958785v2>

Submitted on 7 Jul 2014

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

# Size distribution of amyloid fibrils. Mathematical models and experimental data.

S. Prigent <sup>\*†</sup>    H. W. Haffaf <sup>\*</sup>    H.T. Banks <sup>‡</sup>    M. Hoffmann <sup>§</sup>;  
H.Rezaei <sup>¶</sup>    M. Doumic <sup>\*†</sup>

July 7, 2014

## Abstract

More than twenty types of proteins can adopt misfolded conformations, which can co-aggregate into amyloid fibrils, and are related to pathologies such as Alzheimers disease. This article surveys mathematical models for aggregation chain reactions, and discuss the ability to use them to understand amyloid distributions. Numerous reactions have been proposed to play a role in their aggregation kinetics, though the relative importance of each reaction in vivo is unclear: these include activation steps, with nucleation compared to initiation, disaggregation steps, with depolymerization compared to fragmentation, and additional processes such as filament coalescence or secondary nucleation. We have statistically analysed the shape of the size distribution of prion fibrils, with the specific example of truncated data due to the experimental technique (electron microscopy). A model of polymerization and depolymerization succeeds in explaining this distribution. It is a very plausible scheme though, as evidenced in the review of other mathematical models, other types of reactions could also give rise to the same type of distributions.

**Keywords:** protein aggregation; PrP fiber; Becker-Döring system; statistical test; kernel density estimation.

---

<sup>\*</sup>Inria, Institut National de Recherche en Informatique et Automatique, Rocquencourt, France, and Pierre et Marie Curie University, Paris-Diderot University, CNRS UMR 7598, Paris, France.

<sup>†</sup>Corresponding authors. Email: S.prigent@hotmail.com, marie.doumic@inria.fr.

<sup>‡</sup>Center for Research in Scientific Computation (CRSC), North Carolina State University, Raleigh, N.C., USA

<sup>§</sup>CEREMADE (Centre de REcherche en MATHématique de la DEcision), CNRS-UMR 7534 and CREST. University Paris-Dauphine, Paris, France

<sup>¶</sup>Institut National de Recherche Agronomique, Jouy-en-Josas, France